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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/023,597	12/18/2001	Muralidhara Padigaru	21402-224AD (CURA-524AD)	2896

7590 12/01/2004

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EXAMINER	
LOCKARD, JON MCCLELLAND	
ART UNIT	**PAPER NUMBER**
1647	

DATE MAILED: 12/01/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/023,597	PADIGARU ET AL.	
	Examiner	Art Unit	
	Jon M Lockard	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *20 September 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-52* is/are pending in the application.

4a) Of the above claim(s) *1-4,15-38,40,41 and 43-52* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *5-14,39 and 42* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1-52* are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Sequence Alignment*.

DETAILED ACTION

Election/Restrictions

1. Applicant's election of Group II, claims 5-14, 39, and 42 drawn to nucleic acids of SEQ ID NO:23, vectors and host cells comprising the same, and a method of recombinantly producing the polypeptide of SEQ ID NO:24, in the reply filed on 20 September 2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

2. The restriction requirement is still deemed proper and is therefore made FINAL.

Status of Application, Amendments, And/Or Claims

3. Applicants' amendment filed on 20 September 2004 has been received and entered in full. Claims 1-52 are pending. Claims 5-14, 39, and 42 are under consideration. All other claims are withdrawn from further consideration by the examiner, 37 CFR 1.142(b), as being drawn to a non-elected invention.

Information Disclosure Statement

4. The Information Disclosure Statements (IDS) submitted on 08 April 2002 and 30 April 2003 have been considered by the Examiner.

Specification

5. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed. Applicant is requested to avoid the

use of "novel" in the title, as patents are presumed to be novel and unobvious. The following title is suggested: "G-protein coupled receptor (GPCR) polynucleotides".

Claim Objections

6. Claims 5-14, 39, and 42 are objected to because of the following informalities: Claims 5-14, 39, and 42 encompass non-elected inventions, e.g., SEQ ID NO:2-22 and 26-128 (even) and SEQ ID NO:1-21 and 25-127 (odd) in claims 5 and 8-10. Appropriate correction is required.

7. Claim 9 is objected to because of the following informalities: part (b) of the claim begins with "(b) (b)". Appropriate correction is required.

Claim Rejections - 35 USC § 101 and 35 USC §112

8. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.
>
> The following is a quotation of the first paragraph of 35 U.S.C. 112:
>
> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

9. Claims 5-14, 39, and 42 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific, substantial, and credible asserted utility or a well established utility. Novel biological molecules lack an established utility and must undergo extensive experimentation to determine an appropriate specific, substantial, and credible utility.

10. The instant application discloses a nucleic acid set forth as SEQ ID NO:23 that encodes the protein set forth as SEQ ID NO:24, vectors and host cells comprising the same, pharmaceutical compositions comprising said nucleic acids, and kits comprising the same. The specification asserts that SEQ ID NO:24 is a G protein coupled receptor (GPCR) based on a high degree of homology to known GPCR sequences (see page, lines 25-30). However, the instant specification does not teach any physiologic ligands or functional characteristics of the GPCR set forth in SEQ ID NO:24 or encoded by the disclosed nucleic acid set forth in SEQ ID NO:23. Further, the GPCR comprising SEQ ID NO:24 or encoded by said disclosed nucleic acid has never been expressed in a cell or organism or assayed for functional activity. There is no well-established utility for a specific nucleic acid or amino acid sequence and the specification fails to disclose a specific and substantial utility for the claimed invention.

11. The specification asserts the following as patentable utilities for the claimed DNA (SEQ ID NO:23) encoding the receptor protein of SEQ ID NO:24:

1) as hybridization probes and PCR primers (pg 10, lines 17-20);

2) chromosome mapping (pg 66, line 13 – pg 68, line 14);

3) tissue typing (pg 68, line 16 – pg 69, line 15);

4) prognostic assays (pg 72, line 1 – page 77, line 13);

5) diagnostic assays (pg 70, line 14 – pg 71, line 33);

6) pharmacogenomics (pg 77, line 15 – pg 79, line 6);

7) methods of monitoring treatment (pg 79, line 8 – pg 80, line 16); and

8) prophylactic and/or therapeutic agents for various diseases (pg 80, lines 17-29)

12. These asserted utilities are neither specific nor substantial because they do not identify or reasonably confirm a "real world" context of use. The specification neither identifies the

biological functions of the claimed protein and DNA, nor any diseases that are associated with the claimed molecules. Without any biological activity or link to a disease, such constitutes further research to determine the properties of the claimed GPCR protein or partial peptides, which is insufficient to meet the requirement of 35 USC § 101.

13. These activities and functions are conjectural and are based solely on the identification of the putative protein of SEQ ID NO:24 as being a G-protein coupled receptor (GPCR). While it is credible that SEQ ID NO:24 is a GPCR, its identification as such is not sufficient to establish either a well known, or a specific, substantial and credible utility. There is no ligand identified that binds to it, no signaling pathway with which it is involved, and no disease or disorder correlated with the polypeptide. The use of an orphan receptor to discover its ligand or properties does not constitute a specific, substantial utility. Since the instant specification does not disclose how to use the polypeptide of SEQ ID NO:24, a skilled artisan would not know how to use nucleic acids of SEQ ID NO:23 that encode the polypeptide.

14. The art teaches that the GPCR family is extremely diverse, and that function cannot be predicted merely by identifying a protein as a GPCR. For example, Ji et al., in the Journal of Biological Chemistry 273(28): 17299-17302, teach that there have been nearly 2000 GPCR's reported, which are classifiable into 100 sub families according to sequence homology, ligand structure and receptor function. They further teach that different GPCR superfamily members are capable of sending signals via alternative signal molecules such as Jak2, phospholipase C, or protein kinase C, and that there are other seven transmembrane domain molecules that are not coupled to G proteins at all. Marchese et al. (Genomics 29:335), teach that IL-8 receptor, neuropeptide Y receptor and Somatostatin receptors are all GPCR's. Thus, although the

homology of the GPCR family, especially in the transmembrane domain regions, allows identification of such as both GPCRs and as being evolutionarily related, such is not predictive of function. It is possible that, after further characterization, this protein might be found to have a patentable utility, in which case proteins would have a specific utility, or the protein might be found to be associated with a specific disease.

15. In Brenner v. Manson, 148 U.S.P.Q. 689 (Sup. Ct., 1966), a process of producing a novel compound that was structurally analogous to other compounds which were known to possess anti-cancer activity was alleged to be useful because the compound produced thereby was potentially useful as an anti-tumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. § 101, which requires that an invention must have either an immediately obvious or fully disclosed "real world" utility. The instant claims are drawn to a protein which has undetermined function or biological significance. Until some actual and specific activity or significance can be attributed to the protein identified in the specification as SEQ ID NO:24 or the polynucleotide encoding it (SEQ ID NO:23), the claimed invention is incomplete.

16. Claims 5-14, 39, and 42 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific, substantial and credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to make/use the claimed invention.

17. Furthermore, even if the protein of SEQ ID NO:24 or the DNA of SEQ ID NO:23 that encodes SEQ ID NO:24 were to have a patentable utility, the instant disclosure would not be found to be enabling for the full scope of the claimed invention.

18. Claim 5 recites a polynucleotide or a fragment thereof that encodes a polypeptide or "a portion" thereof that shares at least 85% sequence identity to the polypeptide of SEQ ID NO:24 or complements thereof, claim 9 recites a polynucleotide that shares at least 80% sequence identity to SEQ ID NO:23 or fragments thereof, claim 10 recites a polynucleotide that hybridizes under stringent conditions (See 112¶2 rejection below) to the polynucleotide of SEQ ID NO:23 and complements thereof, and claim 11 recites a polynucleotide that shares at least 80% sequence identity to a polynucleotide that encodes a polypeptide that shares at least 85% sequence identity to the polypeptide of SEQ ID NO:24 and fragments thereof. However, other than the protein of SEQ ID NO:24 and the DNA of SEQ ID NO:23 that encodes the protein, the disclosure fails to provide sufficient guidance and information regarding the structural and functional requirements commensurate in scope with what is encompassed by the instant claims. The disclosure has not shown (1) which portions of SEQ ID NO:24 or SEQ ID NO:23 are critical to the activity of the protein of SEQ ID NO:24 (which is itself unknown); (2) what modifications (e.g., substitutions, deletions, or additions) one can make to SEQ ID NO:24 that will result in protein mutants with the same activity as the protein of SEQ ID NO:24; and (3) any guidance on how to use peptides of SEQ ID NO:24 which would, based on the language of said claims, encompass both active and inactive variants of SEQ ID NO:24. The state of the art is such that the relationship between the sequence of a protein and its activity is not well understood and

unpredictable, and that certain positions in the sequence are critical to the protein's structure/function relationship and can only tolerate only relatively conservative substitutions or no substitutions (See Wells, 1990, Biochemistry 29:8509-8517; Ngo et al., The Protein Folding Problem and Tertiary Structure Prediction, 1994, pp. 492-495).

19. Furthermore, even if the nucleic acid of SEQ ID NO:23 was enabled, the instant disclosure would not be found to be enabling for a pharmaceutical composition comprising the nucleic acid. Since the Instant Specification has not disclosed any disease or disorder correlated with the expression of SEQ ID NO:23 or the protein encoded by it, a skilled artisan would not know how to use a pharmaceutical composition comprising the nucleic acid of SEQ ID NO:23. With respect to this aspect of the rejection, amendment to the claim to read "A composition comprising the nucleic acid molecule of claim 5 and a pharmaceutically-acceptable carrier." would be remedial.

19. Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to the same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of substitutions/deletions on protein structure and function, and the breadth of the claims which fail to recite any structural or functional limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

20. Claims 5-7, 9-14, 39, and 42 are also rejected under 35 USC 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was files, had possession of the claimed invention.

21. The specification discloses a protein of SEQ ID NO:24 and a nucleic acid sequence of SEQ ID NO:23 that encodes the protein of SEQ ID NO:24. However, claim 5 recites a polynucleotide that encodes a polypeptide that shares at least 85% sequence identity to the polypeptide of SEQ ID NO:24 or complements thereof, claim 9 recites a polynucleotide that shares at least 80% sequence identity to SEQ ID NO:23 or fragments thereof, claim 10 recites a polynucleotide that hybridizes under stringent conditions (See 112¶2 rejection below) to the polynucleotide of SEQ ID NO:23 and complements thereof, and claim 11 recites a polynucleotide that shares at least 80% sequence identity to a polynucleotide that encodes a polypeptide that shares at least 85% sequence identity to the polypeptide of SEQ ID NO:24 and fragments thereof.. Claims 6-7, 12-14, 39, and 42 depend, either directly or indirectly, from claim 5. The claims do not require that the proteins and nucleic acids possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of DNA molecules.

22. To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, and any combination thereof. In this case, the only factor present in claims

5, 9, and 11 is a partial structure in the form of a recitation of percent identity. Furthermore, the only factor present in claim 10 is a mere chemical property of the DNA in the form of a recitation of hybridizes to the polynucleotide of SEQ ID NO:23 or a complement thereof. The specification does not identify any particular structure/function correlation or biological activity. The distinguishing characteristics of the claimed genus are not described. The only adequately described species is the polynucleotide set forth as SEQ ID NO:23 and the polypeptide encoded by it (SEQ ID NO:24). Accordingly, the specification does not provide adequate written description of the claimed genus.

23. *Vas-Cath Inc. v. Mahurkar*, 19USPQ2d 1111, clearly states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed*." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116).

24. With the exception of the sequences referred to above, the skilled artisan cannot envision the detailed chemical structure of the encompassed polypeptides and DNA molecules, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The nucleic acid itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

25. One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

26. Therefore, only the polynucleotide set forth as SEQ ID NO:23 and degenerate variants thereof, and the protein encoded by it (SEQ ID NO:24), but not the full breadth of the claims meet the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

Claim Rejections - 35 USC § 112, 2nd paragraph

27. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

28. Claims 5-14, 39, and 42 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

29. Claim 5 is indefinite because it recites the term "mature form". Since neither the art nor the specification provides an unambiguous definition of the term, the metes and bounds of the claim cannot be determined.

30. Claim 5 is further indefinite for reciting "a portion". Without knowing the minimum length of "a portion", the metes and bounds of the claim cannot be determined.

31. Claims 5 and 10-11 are indefinite because the metes and bounds of the term "complement" are not clear from the prior art or the Specification. It is not clear if a full-length or partial complement is intended.

32. Claims 6 and 7 are rejected as being indefinite because it is not clear what is meant by the terms "naturally-occurring allelic nucleic acid variant" in claim 6 and "naturally-occurring polypeptide variant" in claim 7. Since one of ordinary skill in the art would not be able to ascertain whether an isolated sequence represents a naturally-occurring sequence, the metes and bounds of the claims cannot be determined.

33. Claims 9 and 11 are rejected as being indefinite for reciting "fragment". Without knowing the minimum length of the "fragment", the metes and bounds of the claims cannot be determined.

34. Claim 10 is rejected as being indefinite because it is unclear if the "complement" refers to a complement of SEQ ID NO:23 or a complement of a nucleic acid that hybridizes under stringent conditions to SEQ ID NO:23.

35. Claim 10 is rejected as being indefinite as there is no limiting definition of stringent hybridization conditions in the Specification, and the metes and bounds of that which will hybridize are dependent upon the conditions under which the hybridization is performed. The discussion of such at page 18 of the Specification is noted but vague, fails to breathe life and meaning into the term, is exemplary rather than limiting, and thus is insufficient to render the claim definite.

36. Claims 8-9, 12-14, and 39 depend, either directly or indirectly, from claim 5.

Claim Rejections - 35 USC § 102

37. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

38. Claims 5-7 and 9-14 are rejected under 35 U.S.C. 102(e) as being anticipated by Lal et al. (US 2003/0119111 A1, published on 26 June 2003; priority date, 20 March 2000).

39. Lal et al. teach a polynucleotide (SEQ ID NO:35) that encodes a G-protein coupled receptor set forth as SEQ ID NO:14. The disclosed sequence comprises a nucleotide sequence that shares 84% sequence identity with SEQ ID NO:23 of the Instant Application (comprising the coding sequence) and encodes a polypeptide that comprises a polypeptide sequence that shares 87.5% sequence identity with the polypeptide set forth as SEQ ID NO:24 of the Instant Application (See attached Sequence Alignments). It is noted that the terms "comprising a nucleic acid sequence" encoding a polypeptide "comprising an amino acid sequence", for example, as recited in the claims is open language and thus the claims read on the polynucleotide taught by Lal et al. (See also 112¶2 rejections *supra*). The polynucleotide set forth as SEQ ID NO:35 also comprises a fragment (nucleotides 231-269) that shares 100% sequence identity with nucleotides 235-273 of SEQ ID NO:23 of the Instant Application, that encodes a protein that shares 100% sequence identity with amino acid residues 79-98 of SEQ ID NO:24 of the Instant

Application (See attached Sequence Alignments). The polynucleotide set forth as SEQ ID NO:35, which is 84% identical to SEQ ID NO:23, would also hybridize to SEQ ID NO:23 under stringent conditions. Lal et al. also teach the nucleic acids also include fragments and complements of SEQ ID NO:25 (See pg 3, ¶0023 and pg 7, ¶0065). Lal et al. also teach a vector and a host cell comprising the polynucleotides of SEQ ID NO:35 operably linked to a promoter, and a method of producing the receptor protein or fragments thereof (See pg 14, ¶0151 – pg 16, ¶0166). Lastly, Lal et al. teach pharmaceutical compositions comprising the nucleic acids (See pg 23, ¶0212), which by necessity would be in a container. Thus, the reference of Lal et al. meets all the limitations of claims 5-7, 9-14, 39, and 42.

Summary

40. No claim is allowed.

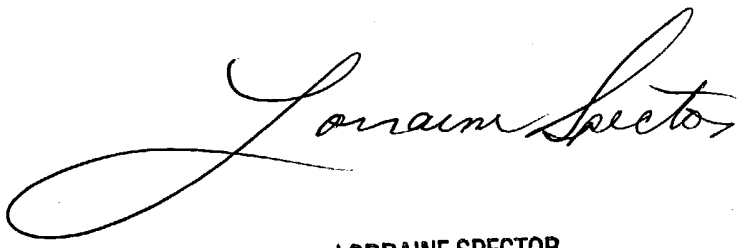
Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Jon M. Lockard, Ph.D.** whose telephone number is **(571) 272-2717**. The examiner can normally be reached on Monday through Friday, 8:00 AM to 6:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Brenda Brumback, Ph.D.** can be reached on **(571) 272-0961**.

The fax number for the organization where this application or proceeding is assigned is **703-872-9306**.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see **http://pair-direct.uspto.gov**. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at **866-217-9197** (toll-free).

JML
November 22, 2004



LORRAINE SPECTOR
PRIMARY EXAMINER

RESULT 10
US-10-343-650A-395
; Sequence 395, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(933)
US-10-343-650A-395

Query Match 71.8%; Score 691.6; DB 13; Length 933;
Best Local Similarity 84.0%; Pred. No. 1.2e-204;
Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy          8 GCCGAGAACTCCTCCTCCGTGACAGAGTTTATCCTCGCAGGCTTAATCCACCAGCCGGGA 67
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Qy         68 CTCCAGGTCCCCGTCTTCTTCCTGTTTCTAGGTTTCTACGCGGTCACGGTGGTGGGGAAC 127
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Qy        128 CTGGGCTTGATAACCCTGATAGGGCTCAACTCTCGCCTGCATATCCCCATGTACTTTTTC 187
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Qy        188 CCCTTCAACTTGTCCCTCGTAGATTTTAGTTTCTCTACGACCATCATTCCCAAAATGCTG 247
              |  || ||| | ||    ||||||| ||||||| || ||||||| ||||||||||||
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Db        244 ATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATGACTCAGCTCTTC 303

Qy        308 TTCTTCTGTTTCTTTGTCTTTTCTGAGTCCTTCATCCTGTCGGCGATGGTGGAGGACCGC 367
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Qy        368 TACGTGGGCATCTGTAACCCACTGTTGTACACGATCACCATGTCTCCCCAGGTGTGTTTG 427
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Db        364 TACGTGGCCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTG 423

Qy        428 CTCCTTTTACTGGGTGTCTACGGGATGGGGGTTTTTGGGGCTGTGGCTCATACAGGAAAT 487
              |||||||| |||||| ||| |||||||||| ||  |||||| |||| || |||||||
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Qy        488 ATAGTGTTTCTCACCTTTTGTGCAGACAACCTTGTCAATCACTACATGTGTGACATCCTT 547
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Qy        548 CCCCTTCTTGAGCTCTCCTGCAACGGCTCTTACATAAATGTCCTGGTCATCTTTATTGTT 607
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Db        544 CCTCTCCTTGAGCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTG 603

Qy        608 GTGACCGTTGGCATTGGGGTGCCCATTGTTGCCGTTTTTATCTCTTATGGTTTTATTCTT 667
              ||| | |||| | ||||  |||||||||||  | || |||||  |||||||    | || ||
Db        604 GTGGCTGTTGACGTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTCATCCTC 663

Qy        668 TCCAGCATTCTCCGCGTTAGTTCTGCTGAGGGCAGGTCTAAAGCCTTCAGTAGCTGCAGC 727
              |||||||||||| | |    |||||| | || |||||||| ||||||| ||||  |||||
Db        664 TCCAGCATTCTACACAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAGT 723

Qy        728 TCCTACATAATTGCAGTTTCTCTTTTCTTTGGGTCAGGAGCTTTTACGTACCTCAAACCC 787
              ||| |||||||| ||||||||||||||||||| || || ||||| | ||| |||||||||
Db        724 TCCCACATAATTGTAGTTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTCAAACCC 783

Qy        788 CCTTCCATTTTACCCCTGGACCAGGGGAAAGTGTCCTCCCTGTTCTATACCACTGTGGTG 847
              | ||||||  | |||| || || ||||||||||||||||||||||||    | ||
Db        784 CTTTCCATCCTGCCCCCTGAGCAAGGGAAAGTGTCCTCCCTGTTCTATACCATAATAGTC 843

Qy        848 CCCATGTTTAACCCATTAATCTACAGCCTGAGGAATAAGGATGTCAAACTTGCCCTGAAG 907
              ||| |||| |||||||||||||| |||||| ||||||||||| ||||||||| |
Db        844 CCCGTGTTAAACCCATTAATCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGG 903

Qy        908 AGAACCTTTTCCAGAATAAGCTTTTCTTAA 937
              ||||| ||   ||||| || |||||||| |
Db        904 AGAACTTTGGGCAGAAAAATCTTTTCTTAA 933
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RESULT 11
US-10-220-382-35
; Sequence 35, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROWSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/10/220,382
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119111A1 7472439CB1
US-10-220-382-35

Query Match 71.8%; Score 691.6; DB 15; Length 933;
Best Local Similarity 84.0%; Pred. No. 1.2e-204;
Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy          8 GCCGAGAACTCCTCCTCCGTGACAGAGTTTATCCTCGCAGGCTTAATCCACCAGCCGGGA 67
              || |  ||  ||| || ||||||||||||||||||| ||||||| ||||||||||||
Db          4 GCAGCCAAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGGGA 63

Qy         68 CTCCAGGTCCCCGTCTTCTTCCTGTTTCTAGGTTTCTACGCGGTCACGGTGGTGGGGAAC 127
              || | | ||||| |||||||||||||||| |||||||| ||||||| ||||||||||||
Db         64 CTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAAC 123
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Qy        128 CTGGGCTTGATAATCCTGATAGGGCTCAACTCTCGCCTGCATATCCCCATGTACTTTTTC 187
              ||||||||||||| |||||| ||||| |||||||| |||||| | ||||||||||| |||
Db        124 CTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTACTTCTTC 183

Qy        188 CCCTTCAACTTGTCCCTCGTAGATTTTAGTTTCTCTACGACCATCATTCCCAAAATGCTG 247
              |  || ||| | ||  |  |||||||  ||||||| || ||||||| ||||||||||||
Db        184 CTTTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTG 243

Qy        248 ATGAGTTTTGTCTCAAGGAAGAACATTATTTCCTTCACAGGGTGTATGAGTCAGTTCTTC 307
              |||||||||||||||||||||||||||| |||||||||||||||||||| |||| |||||
Db        244 ATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATGACTCAGCTCTTC 303

Qy        308 TTCTTCTGTTTCTTTGTCTTTTCTGAGTCCTTCATCCTGTCGGCGATGGTGGAGGACCGC 367
              ||||||| |||||||||||||||||||||||||||||||| ||||||| | | ||||||
Db        304 TTCTTCTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTATGACCGC 363

Qy        368 TACGTGGGCATCTGTAACCCACTGTTGTACACGATCACCATGTCTCCCCAGGTGTGTTTG 427
              ||||||| |||||||||||||||||||||||||   |||||||||||  ||||||||||||
Db        364 TACGTGGCCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTG 423

Qy        428 CTCCTTTTACTGGGTGTCTACGGGATGGGGGTTTTTGGGGCTGTGGCTCATACAGGAAAT 487
              |||||||| |||||| ||| |||||||||  ||  ||||||  |||| || ||||||||
Db        424 CTCCTTTTGTTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCCACACAGGAAGC 483

Qy        488 ATAGTGTTTCTCACCTTTTGTGCAGACAACCTTGTCAATCACTACATGTGTGACATCCTT 547
              ||| ||   || ||||| |||| |||||||||||||||| | ||||||||||||||||
Db        484 ATAATGAACCTGACCTTCTGTGCTGACAACCTTGTCAATCATTTCATGTGTGACATCCTT 543

Qy        548 CCCCTTCTTGAGCTCTCCTGCAACGGCTCTTACATAAATGTCCTGGTCATCTTTATTGTT 607
              || || |||||||||||||||||| |||||||||  |||| |||||  ||||||||||
Db        544 CCTCTCCTTGAGCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTG 603

Qy        608 GTGACCGTTGGCATTGGGGTGCCCATTGTTGCCGTTTTTATCTCTTATGGTTTTATTCTT 667
              ||| | |||| | |||| |||||||||| | || ||||| |||||||     | || ||
Db        604 GTGGCTGTTGACGTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTCATCCTC 663

Qy        668 TCCAGCATTCTCCGCGTTAGTTCTGCTGAGGGCAGGTCTAAAGCCTTCAGTAGCTGCAGC 727
              |||||||||||  |  |||||| | || |||||||| |||||||| |||| |||||
Db        664 TCCAGCATTCTACACAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAGT 723

Qy        728 TCCTACATAATTGCAGTTTCTCTTTTCTTTGGGTCAGGAGCTTTTACGTACCTCAAACCC 787
              ||| |||||||| |||||||||||||||||| || || ||||| | ||| |||||||||
Db        724 TCCCACATAATTGTAGTTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTCAAACCC 783

Qy        788 CCTTCCATTTTACCCCTGGACCAGGGGAAAGTGTCCTCCCTGTTCTATACCACTGTGGTG 847
              | ||||||  | ||||| || ||||||||||||||||||||||||||||||  | ||
Db        784 CTTTCCATCCTGCCCCTCGAGCAAGGGAAAGTGTCCTCCCTGTTCTATACCATAATAGTC 843

Qy        848 CCCATGTTTAACCCATTAATCTACAGCCTGAGGAATAAGGATGTCAAACTTGCCCTGAAG 907
              ||| |||| |||||||||||||| ||| ||||||| |||||||||||| |||||||| |
Db        844 CCCGTGTTAAACCCATTAATCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGG 903

Qy        908 AGAACCTTTTCCAGAATAAGCTTTTCTTGA 937
              ||||| ||   |||| || |||||||| |
Db        904 AGAACTTTGGGCAGAAAAATCTTTTCTTAA 933
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RESULT 12
US-10-017-161-749
; Sequence 749, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 084335/0152
;  CURRENT APPLICATION NUMBER: US/10/017,161
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: JP 2001/246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2430
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 749
;   LENGTH: 1336
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: source
;   LOCATION: (1)..(1336)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)..(1136)
US-10-017-161-749

  Query Match             68.3%;  Score 657.4;  DB 15;  Length 1336;
  Best Local Similarity   80.2%;  Pred. No. 7.4e-194;
  Matches  772;  Conservative    0;  Mismatches  191;  Indels    0;  Gaps    0;

Qy          1 AATGGCTGCCGAGAACTCCTCCTCCGTGACAGAGTTTATCCTCGCAGGCTTAATCCACCA 60
              |||||||| |||| |||||| |||||| |||||||||||||||||||||    ||||
Db        200 AATGGCTGCTGAGAATTCCTCCTTCGTGACACAGTTTATCCTCGCAGGCTTAACTGACCA 259

Qy         61 GCCGGGACTCCAGGTCCCCGTCTTCTTCCTGTTTCTAGGTTTCTACGCGGTCACGGTGGT 120
              |||||| |||| |||||||||||||||||||||||||||||| |||||| |||| |||||
Db        260 ACCGGGAGTCCAGATCCCCCTCTTCTTCCTGTTTCTAGGCTTCTACGTGGTCACTGTGGT 319

Qy        121 GGGGAACCTGGGCTTGATAATCCTGATAGGGCTCAACTCTCGCCTGCATATCCCCATGTA 180
              |||||||||||||||| |||||| |||||||||||| | |||| | ||| ||||
Db        320 GGGGAACCTGGGCTTGATAACCCTGATAAGGCTCAACTCTCACTTGCACACCCCTATGTA 379

Qy        181 CTTTTTCCCCTTCAACTTGTCCCTCGTAGATTTTAGTTTCTCTACGACCATCATTCCCAA 240
              ||| |||| ||  |||||||| || |||||||  | |  || |    |||| ||||||
Db        380 CTTCTTCCTCTATAACTTGTCCTTCATAGATTTCTGCTATTCCAGTGTTATCACTCCCAA 439

Qy        241 AATGCTGATGAGTTTTGTCTCAAGGAAGAACATTATTTCCTTCACAGGGTGTATGAGTCA 300
              |||||||||||||||||| || |||||||| |||| | |||||||||||||||||||||
Db        440 AATGCTGATGAGCTTTGTCTTAAAGAAGAACAGCATCTCCTACGCAGGGTGTATGACTCA 499

Qy        301 GTTCTTCTTCTTCTGTTTCTTTGTCTTTTCTGAGTCCTTCATCCTGTCGGCGATGGTGGA 360
              | |||||||||  |||||||  | |||||||||||||||||||| || |||| | |
Db        500 GCTCTTCTTCTTTCTTTTCTTTGTTGTCTCTGAGTCCTTCATCCTGTCAGCAATGGCGTA 559

Qy        361 GGACCGCTACGTGGGCATCTGTAACCCACTGTTGTACACGATCACCATGTCTCCCCAGGT 420
              |||||||| |||| |||||||||||||||||||||||||||| |||||||||||||||
Db        560 TGACCGCTATGTGGCCATCTGTAACCCACTGTTGTACATGGTCACCATGTCTCCCCAGGT 619

Qy        421 GTGTTTGCTCCTTTTACTGGGTGTCTACGGGATGGGGGTTTTTGGGGCTGTGGCTCATAC 480
              |||||| |||||||| |||||||| |||||||| ||  |||||  |||| || ||
Db        620 GTGTTTTCTCCTTTTGTTGGGTGTCTATGGGATGGGGTTTGCTGGGGCCATGGCCCACAC 679

Qy        481 AGGAAATATAGTGTTTCTCACCTTTTGTGCAGACAACCTTGTCAATCACTACATGTGTGA 540
              ||    ||  ||  | | ||||| |||||  | |||||||||| ||||||||||||||
Db        680 AGCGTGCATGATGGGTGTGACCTTCTGTGCCAATAACCTTGTCAACCACTACATGTGTGA 739

Qy        541 CATCCTTCCCCTTCTTGAGCTCTCCTGCAAGGGCTCTTACATAAATGTCCTGGTCATCTT 600
              |||||||||||||||||||    | |||| |||| | ||  |||||  || ||  | ||
Db        740 CATCCTTCCCCTTCTTGAGTGTGCTTGCACCAGCACCTATGTGAATGAGCTTGTAGTGTT 799

Qy        601 TATTGTTGTGACCGTTGGCATTGGGGTGCCCATTGTTGCCGTTTTTATCTCTTATGGTTT 660
              | ||||||||  | |||  |||||| |||||||  || | || || || |||| | |
Db        800 TGTTGTTGTGGGCATTGATATTGGTGTGCCCACAGTCACCATCTTCATTTCCTATGCTCT 859

Qy        661 TATTCTTTCCAGCATTCTCCGCGTTAGTTCTGCTGAGGGCAGGTCTAAAGCCTTCAGTAG 720
              |||||  |||||||  ||| | ||  |||  | ||||||||||| |||||||||| |
Db        860 CATTCTCTCCAGCATCTTCCACATTGATTCCACGGAGGGCAGGTCCAAAGCCTTCAGCAC 919

Qy        721 CTGCAGCTCCTACATAATTGCAGTTTCTCTTTTCTTTGGGTCAGGAGCTTTTACGTACCT 780
              |||||||||| |||||||||||||||||||||||||||||||||||| || | ||||||
Db        920 CTGCAGCTCCCACATAATTGCAGTTTCTCTGTTCTTTGGGTCAGCAGCATTCATGTACCT 979

Qy        781 CAAACCCCCTTCCATTTTACCCCTGGACCAGGGGAAAGTGTCCTCCCTGTTCTATACCAC 840
              |||||||  |||  |||||  ||  |||||||  || ||||| ||||| ||||||||||
Db        980 CAAACCCTTTTCTCTTTTAGCTATGAACCAGGGCAAGGTGTCTTCCCTATTCTATACCAC 1039
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Db        778 AAACCCCTTTCCATCCTGCCCCTCGAGCAAGGGAAAGTGTCCTCCCTGTTCTATACCATA 837

Qy        281 ValValProMetPheAsnProLeuIleTyrSerLeuArgAsnLysAspValLysLeuAla 300

Db        838 ATAGTCCCCGTGTTAAACCCATTAATCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCC 897

Qy        301 LeuLysArgThrPheSerArgIleSerPheSer 311

Db        898 CTGAGGAGAACTTTGGGCAGAAAAATCTTTTCT 930

RESULT 4
US-10-343-650A-395
; Sequence 395, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
;  APPLICANT: HAGA, TATSUYA
;  TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
;  FILE REFERENCE: 31671-186347
;  CURRENT APPLICATION NUMBER: US/10/343,650A
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: JP 2000/237818
;  PRIOR FILING DATE: 2000-08-04
;  PRIOR APPLICATION NUMBER: JP 2001/34434
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 694
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
;   LENGTH: 933
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(933)
US-10-343-650A-395

Alignment Scores:
Pred. No.:              2.59e-116       Length:         933
Score:                  1273.50         Matches:        250
Percent Similarity:     87.46%          Conservative:   22
Best Local Similarity:  80.39%          Mismatches:     38
Query Match:            80.75%          Indels:         1
DB:                     13              Gaps:           1

US-10-023-597-24 (1-311) x US-10-343-650A-395 (1-933)

Qy          1 MetAlaAlaGluAsnSerSerSerValThrGluPheIleLeuAlaGlyLeuIleHisGln 20

Db          1 ATGGCAGCCAAAAAC---TCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAG 57

Qy         21 ProGlyLeuGlnValProValPhePheLeuPheLeuGlyPheTyrAlaValThrValVal 40

Db         58 CCGGGACTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTTCTACACGGTCACCGTGGTG 117

Qy         41 GlyAsnLeuGlyLeuIleIleLeuIleGlyLeuAsnSerArgLeuHisIleProMetTyr 60

Db        118 GGGAACCTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTAC 177

Qy         61 PhePheProPheAsnLeuSerLeuValAspPheSerPheSerThrThrIleIleProLys 80

Db        178 TTCTTCCTTTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAA 237

Qy         81 MetLeuMetSerPheValSerArgLysAsnIleIleSerPheThrGlyCysMetSerGln 100

Db        238 ATGCTGATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATGACTCAG 297

Qy        101 PhePhePhePheCysPhePheValPheSerGluSerPheIleLeuSerAlaMetValGlu 120

Db        298 CTCTTCTTCTTCTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTAT 357

Qy        121 AspArgTyrValGlyIleCysAsnProLeuLeuTyrThrIleThrMetSerProGlnVal 140

Db        358 GACCGCTACGTGGCCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTG 417

Qy        141 CysLeuLeuLeuLeuGlyValTyrGlyMetGlyValPheGlyAlaValAlaHisThr 160

Db        418 TGTTTGCTCCTTTTGTTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCCACACA 477

Qy        161 GlyAsnIleValPheLeuThrPheCysAlaAspAsnLeuValAsnHisTyrMetCysAsp 180

Db        478 GGAAGCATAATGAACCTGACCTTCTGTGCTGACAACCTTGTCAATCATTTCATGTGTGAC 537

Qy        181 IleLeuProLeuLeuGluLeuSerCysAsnGlySerTyrIleAsnValLeuValIlePhe 200

Db        538 ATCCTTCCTCTCCTTGAGCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTT 597

Qy        201 IleValValThrValGlyIleGlyValProIleValAlaValPheIleSerTyrGlyPhe 220

Db        598 ATTGTGGTGGCTGTTGACGTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTC 657

Qy        221 IleLeuSerSerIleLeuArgValSerSerAlaGluGlyArgSerLysAlaPheSerSer 240

Db        658 ATCCTCTCCAGCATTGTACACAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACT 717

Qy        241 CysSerSerTyrIleIleAlaValSerLeuPhePheGlySerGlyAlaPheThrTyrLeu 260

Db        718 TGCAGTTCCCACATAATTGTAGTTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTC 777

Qy        261 LysProProSerIleLeuProLeuAspGlnGlyLysValSerSerLeuPheTyrThrThr 280

Db        778 AAACCCCTTTCCATCCTGCCCCTCGAGCAAGGGAAAGTGTCCTCCCTGTTCTATACCATA 837

Qy        281 ValValProMetPheAsnProLeuIleTyrSerLeuArgAsnLysAspValLysLeuAla 300

Db        838 ATAGTCCCCGTGTTAAACCCATTAATCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCC 897

Qy        301 LeuLysArgThrPheSerArgIleSerPheSer 311

Db        898 CTGAGGAGAACTTTGGGCAGAAAAATCTTTTCT 930

RESULT 5
US-10-220-382-35
; Sequence 35, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  SHIH, Leo L.
;  APPLICANT:  TRIBOULEY, Catherine
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  YANG, Junming
;  APPLICANT:  HARLAND, Lee
;  APPLICANT:  WALSH, Roderick T.
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  BOROWSKY, Mark L.
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0044 PCT
;  CURRENT APPLICATION NUMBER: US/10/220,382
;  CURRENT FILING DATE:  2001-03-01
;  PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
;  PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 35
;   LENGTH: 933
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
```

; OTHER INFORMATION: Incyte ID No. US20030119111A1 7472439CB1
US-10-220-382-35

Alignment Scores:

Pred. No.:	2.59e-116	Length:	933
Score:	1273.50	Matches:	250
Percent Similarity:	87.46%	Conservative:	22
Best Local Similarity:	80.39%	Mismatches:	38
Query Match:	80.75%	Indels:	1
DB:	15	Gaps:	1

US-10-023-597-24 (1-311) x US-10-220-382-35 (1-933)

```
Qy          1 MetAlaAlaGluAsnSerSerSerValThrGluPheIleLeuAlaGlyLeuIleHisGln 20
              |||||||||:::|||   |||||||||||||||||||||||||   ||||||   ||||||
Db          1 ATGGCAGCCAAAAAC---TCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAG 57

Qy         21 ProGlyLeuGlnValProValPhePheLeuPheLeuGlyPheTyrAlaValThrValVal 40
              |||||||||:::::|||:::|||||||||||||||||||||||||   ||||||||||||
Db         58 CCGGGACTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTTCTACACGGTCACCGTGGTG 117

Qy         41 GlyAsnLeuGlyLeuIleIleLeuIleGlyLeuAsnSerArgLeuHisIleProMetTyr 60
              ||||||||||||||||||   ||||||||||||||||||   ||||||   |||||||||
Db        118 GGGAACCTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTAC 177

Qy         61 PhePheProPheAsnLeuSerLeuValAspPheSerPheSerThrThrIleIleProLys 80
              ||||||   ||||||||||||||:::||||||   ||||||||||||||   ||||||
Db        178 TTCTTCCTTTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAA 237

Qy         81 MetLeuMetSerPheValSerArgLysAsnIleIleSerPheThrGlyCysMetSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        238 ATGCTGATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATGACTCAG 297

Qy        101 PhePhePhePheCysPhePheValPheSerGluSerPheIleLeuSerAlaMetValGlu 120
              |||||||||||||||||||   ||||||||||||||||||||||||||||
Db        298 CTCTTCTTCTTCTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTAT 357

Qy        121 AspArgTyrValGlyIleCysAsnProLeuLeuTyrThrIleThrMetSerProGlnVal 140
              ||||||||||||   ||||||||||||||||||||||||:::|||||||   ||||||
Db        358 GACCGCTACGTGGCCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTG 417

Qy        141 CysLeuLeuLeuLeuGlyValTyrGlyMetGlyValPheGlyAlaValAlaHisThr 160
              |||||||||||||||||||   ||||||||||||   ||||||:::|||||||||
Db        418 TGTTTGCTCCTTTTGTTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCCACACA 477

Qy        161 GlyAsnIleValPheLeuThrPheCysAlaAspAsnLeuValAsnHisTyrMetCysAsp 180
              |||:::|||:::   ||||||||||||||||||||||||||||||:::|||||||||
Db        478 GGAAGCATAATGAACCTGACCTTCTGTGCTGACAACCTTGTCAATCATTTCATGTGTGAC 537

Qy        181 IleLeuProLeuLeuGluLeuSerCysAsnGlySerTyrIleAsnValLeuValIlePhe 200
              |||||||||||||||||||||||||||||   |||||:::|||   |||||||:::|||
Db        538 ATCCTTCCTCTCCTTGAGCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTT 597

Qy        201 IleValValThrValGlyIleGlyValProIleValAlaValPheIleSerTyrGlyPhe 220
              |||||||||   |||   :::|||:::|||||||||   ||||||||||||||||
Db        598 ATTGTGGTGGCTGTTGACGTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTC 657

Qy        221 IleLeuSerSerIleLeuArgValSerSerAlaGluGlyArgSerLysAlaPheSerSer 240
              ||||||||||||||||||   ||||||   ||||||||||||||||||||||||||:::
Db        658 ATCCTCTCCAGCATTCTACACAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACT 717

Qy        241 CysSerSerTyrIleIleAlaValSerLeuPhePheGlySerGlyAlaPheThrTyrLeu 260
              |||||||||:::||||||   ||||||||||||||||||||||||||||||   ||||||
Db        718 TGCAGTTCCCACATAATTGTAGTTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTC 777

Qy        261 LysProProSerIleLeuProLeuAspGlnGlyLysValSerSerLeuPheTyrThrThr 280
              ||||||   ||||||||||||||:::||||||||||||||||||||||||||||||||
Db        778 AAACCCCTTTCCATCCTGCCCCTCGAGCAAGGGAAAGTGTCCTCCCTGTTCTATACCATA 837

Qy        281 ValValProMetPheAsnProLeuIleTyrSerLeuArgAsnLysAspValLysLeuAla 300
              :::||||||:::   ||||||||||||||||||||||||||||||||||||||:::|||
Db        838 ATAGTCCCCGTGTTAAACCCATTAATCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCC 897

Qy        301 LeuLysArgThrPheSerArgIleSerPheSer 311
              |||:::||||||   |||   ||||||
Db        898 CTGAGGAGAACTTTGGGCAGAAAAATCTTTTCT 930
```

RESULT 6
US-10-017-161-325
; Sequence 325, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 325
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1333)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1133)
US-10-017-161-325

Alignment Scores:

Pred. No.:	4.32e-116	Length:	1333
Score:	1273.50	Matches:	250
Percent Similarity:	87.46%	Conservative:	22
Best Local Similarity:	80.39%	Mismatches:	38
Query Match:	80.75%	Indels:	1
DB:	15	Gaps:	1

US-10-023-597-24 (1-311) x US-10-017-161-325 (1-1333)

```
Qy          1 MetAlaAlaGluAsnSerSerSerValThrGluPheIleLeuAlaGlyLeuIleHisGln 20
              |||||||||:::|||   |||||||||||||||||||||||||   ||||||   ||||||
Db        201 ATGGCAGCCAAAAAC---TCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAG 257

Qy         21 ProGlyLeuGlnValProValPhePheLeuPheLeuGlyPheTyrAlaValThrValVal 40
              |||||||||:::::|||:::|||||||||||||||||||||||||   ||||||||||||
Db        258 CCGGGACTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTTCTACACGGTCACCGTGGTG 317

Qy         41 GlyAsnLeuGlyLeuIleIleLeuIleGlyLeuAsnSerArgLeuHisIleProMetTyr 60
              ||||||||||||||||||   ||||||||||||||||||   ||||||   |||||||||
Db        318 GGGAACCTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTAC 377

Qy         61 PhePheProPheAsnLeuSerLeuValAspPheSerPheSerThrThrIleIleProLys 80
              ||||||   ||||||||||||||:::||||||   ||||||||||||||   ||||||
Db        378 TTCTTCCTTTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAA 437

Qy         81 MetLeuMetSerPheValSerArgLysAsnIleIleSerPheThrGlyCysMetSerGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        438 ATGCTGATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATGACTCAG 497

Qy        101 PhePhePhePheCysPhePheValPheSerGluSerPheIleLeuSerAlaMetValGlu 120
              |||||||||||||||||||   ||||||||||||||||||||||||||||
Db        498 CTCTTCTTCTTCTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTAT 557

Qy        121 AspArgTyrValGlyIleCysAsnProLeuLeuTyrThrIleThrMetSerProGlnVal 140
              ||||||||||||   ||||||||||||||||||||||||:::|||||||   ||||||
Db        558 GACCGCTACGTGGCCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTG 617

Qy        141 CysLeuLeuLeuLeuGlyValTyrGlyMetGlyValPheGlyAlaValAlaHisThr 160
              |||||||||||||||||||   ||||||||||||   ||||||:::|||||||||
```

; SEQ ID NO 50
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-886-855-50

Query Match 4.0%; Score 39; DB 9; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 273
||||||||||||||||||||||||||||||||||||||||
Db 231 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 269

RESULT 13
US-09-804-291-50
; Sequence 50, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-291-50

Query Match 4.0%; Score 39; DB 10; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 273
||||||||||||||||||||||||||||||||||||||||
Db 231 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 269

RESULT 14
US-10-343-650A-395
; Sequence 395, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(933)
US-10-343-650A-395

Query Match 4.0%; Score 39; DB 13; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 273
||||||||||||||||||||||||||||||||||||||||
Db 231 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 269

RESULT 15
US-10-220-382-35
; Sequence 35, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROWSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/10/220,382
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119111A1 7472439CB1
US-10-220-382-35

Query Match 4.0%; Score 39; DB 15; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 273
||||||||||||||||||||||||||||||||||||||||
Db 231 TCCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACAT 269

Search completed: September 30, 2004, 10:01:34
Job time : 562 secs

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Qy          79 ProLysMetLeuMetSerPheValSerArgLysAsnIleIleSerPheThrGlyCysMet 98
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 CCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATG 291
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RESULT 11
US-10-220-382-35
; Sequence 35, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROWSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/10/220,382
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119111A1 7472439CB1
US-10-220-382-35

Alignment Scores:

Pred. No.:	6.36e-10	Length:	933
Score:	20.00	Matches:	20
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.43%	Indels:	0
DB:	15	Gaps:	0

US-10-023-597-24 (1-311) x US-10-220-382-35 (1-933)

```
Qy          79 ProLysMetLeuMetSerPheValSerArgLysAsnIleIleSerPheThrGlyCysMet 98
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 CCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATG 291
```

RESULT 12
US-10-005-041A-13
; Sequence 13, Application US/10005041A
; Publication No. US20030232331A1
; GENERAL INFORMATION:
; APPLICANT: Casman, Stacie J
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gilbert, Jennifer A
; APPLICANT: Mayotte, Jane E
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine AM
; APPLICANT: Dickinson, Kevin S
; APPLICANT: Ballinger, Robert A
; APPLICANT: Wolenc, Adam R
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-215
; CURRENT APPLICATION NUMBER: US/10/005,041A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/251,459
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/259,007
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-041A-13

Alignment Scores:

Pred. No.:	6.5e-10	Length:	953
Score:	20.00	Matches:	20
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.43%	Indels:	0
DB:	16	Gaps:	0

US-10-023-597-24 (1-311) x US-10-005-041A-13 (1-953)

```
Qy          79 ProLysMetLeuMetSerPheValSerArgLysAsnIleIleSerPheThrGlyCysMet 98
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         247 CCCAAAATGCTGATGAGTTTTGTCTCAAGGAAGAACATCATTTCCTTCACAGGGTGTATG 306
```

RESULT 13
US-10-024-399-1
; Sequence 1, Application US/10024399
; Publication No. US20030100491A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Colman, Steven D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Ballinger, Robert A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Casman, Stacie J.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-224AE
; CURRENT APPLICATION NUMBER: US/10/024,399
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,635
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/259,743
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/295,327
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/261,498
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/263,689
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/267,464
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/271,021
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/275,946